L Number	Hits	Search Text	DB	Time stamp
1	133	coxsackievirus near3 adenovirus near3 receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:24
2	626	car and adenovirus	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
3	4	cxadr	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
4	0	cvb3 adj binding adj protein	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
5	731	(coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
6	483	((coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)) and (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:26
7	77107	pig or porcine	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:27
8	0	(coxsackievirus near3 adenovirus near3 receptor) near10 (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:27
9	29	PCAR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:28
10	0	PCAR AND ADENOVIRUS	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:29
11	456	(((coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)) and (pig or porcine)) AND ("NUCLEIC ACID" OR DNA)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:32
12	0	(coxsackievirus near3 adenovirus near3 receptor) NEAR5 (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:32
13	154	(pig or porcine) NEAR5 CAR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:33
14	1	((pig or porcine) NEAR5 CAR) AND COXSACKIEVIRUS	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:34
15	0	(pig or porcine) NEAR5 CVB3	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:35
16	0	(pig or porcine) NEAR5 CXADR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:35

(FILE 'HOME' ENTERED AT 14:04:56 ON 07 AUG 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 14:07:29 ON 07 AUG 2003

L1	834	S	COXSACKIEVIRUS(3A)ADENOVIRUS
L2	628	S	L1(3A)RECEPTOR
L3	5	S	CXADR
L4	1178	S	CAR AND ADENOVIRUS
L5	572	S	L4 AND COXSACKIEVIRUS
L6	1115	S	CVB3
L7	5	S	CVB3 BINDING PROTEIN
L8	2374	S	L2 OR L4 OR L3 OR L6
L9	27	S	L8 AND (PIG OR PORCINE)
L10	10		DUP REM L9 (17 DUPLICATES REMOVED)

NiceProt View of Swiss-Prot: P78310

Printer-friendly view | Quick BlastP search

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**CXAR_HUMAN**
Primary accession number	**P78310**
Secondary accession number	O00694
Entered in Swiss-Prot in	Release 39, May 2000
Sequence was last modified in	Release 39, May 2000
Annotations were last modified in	Release 42, September 2003

Name and origin of the protein

Protein name	**Coxsackievirus and adenovirus receptor [Precursor]**
Synonyms	**Coxsackievirus B-adenovirus receptor** **hCAR** **CVB3 binding protein**
Gene name	**CXADR** or **CAR**
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=97190109; PubMed=9036860; [NCBI, ExPASy, EBI, Israel, Japan]
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[2] SEQUENCE FROM NUCLEIC ACID.
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Tomko R.P., Xu R., Philipson L.;
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Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE FROM NUCLEIC ACID.
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[6] SEQUENCE FROM NUCLEIC ACID.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Comments

- ***FUNCTION***: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
- ***SUBCELLULAR LOCATION***: Type I membrane protein.
- ***SIMILARITY***: Contains 2 immunoglobulin-like C2-type domains.

Copyright

Cross-references

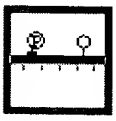
EMBL	Y07593; CAA68868.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U90716; AAC51234.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169366; AAF05908.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169360; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169361; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169362; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169363; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169364; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169365; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]

	AF200465; AAF24344.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF242865; AAG01088.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF242862; AAG01088.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] AF242864; AAG01088.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence] BC003684; AAH03684.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] BC010536; AAH10536.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PDB	1EAJ; 13-JUL-01. [ExPASy / RCSB] 1F5W; 08-NOV-00. [ExPASy / RCSB] 1KAC; 24-NOV-99. [ExPASy / RCSB] Detailed list of linked structures.
Genew	HGNC:2559; CXADR.
CleanEx	HGNC:2559; CXADR.
MIM	602621 [NCBI / EBI].
GeneCards	CXADR.
GeneLynx	CXADR; Homo sapiens.
GO	GO:0005887; Cellular component: integral to plasma membrane *(traceable author statement)*. GO:0004872; Molecular function: receptor activity *(traceable author statement)*.
SOURCE	CXADR; Homo sapiens.
Ensembl	P78310; Homo sapiens. [Entry / Contig view]
InterPro	IPR007110; Ig-like. IPR003598; Ig_c2. Graphical view of domain structure.
Pfam	PF00047; ig; 2.
SMART	SM00408; IGc2; 1.
PROSITE	PS50835; IG_LIKE; 2.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	P78310.
ProtoNet	P78310.
ProtoMap	P78310.
PRESAGE	P78310.
DIP	P78310.
ModBase	P78310.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Immunoglobulin domain; **Receptor**; **Transmembrane**; **Glycoprotein**; **Signal**; **Repeat**; **3D-structure**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description
SIGNAL	1	19	19	*POTENTIAL.*

CHAIN	20	365	346	COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
DOMAIN	20	237	218	EXTRACELLULAR (*POTENTIAL*).
TRANSMEM	238	258	21	*POTENTIAL*.
DOMAIN	259	365	107	CYTOPLASMIC (*POTENTIAL*).
DOMAIN	20	134	115	IG-LIKE C2-TYPE 1.
DOMAIN	141	228	88	IG-LIKE C2-TYPE 2.
DISULFID	41	120		*BY SIMILARITY*.
DISULFID	162	212		*BY SIMILARITY*.
CARBOHYD	106	106		N-LINKED (GLCNAC...) (*POTENTIAL*).
CARBOHYD	201	201		N-LINKED (GLCNAC...) (*POTENTIAL*).

Sequence information

Length: **365 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40029 Da** [This is the MW of the unprocessed precursor]

CRC64: **AB01C6346CB7FE64** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
         |          |          |          |          |          |
MALLLCFVLL CGVVDFARSL SITTPEEMIE KAKGETAYLP CKFTLSPEDQ GPLDIEWLIS

        70         80         90        100        110        120
         |          |          |          |          |          |
PADNQKVDQV IILYSGDKIY DDYYPDLKGR VHFTSNDLKS GDASINVTNL QLSDIGTYQC

       130        140        150        160        170        180
         |          |          |          |          |          |
KVKKAPGVAN KKIHLVVLVK PSGARCYVDG SEEIGSDFKI KCEPKEGSLP LQYEWQKLSD

       190        200        210        220        230        240
         |          |          |          |          |          |
SQKMPTSWLA EMTSSVISVK NASSEYSGTY SCTVRNRVGS DQCLLRLNVV PPSNKAGLIA

       250        260        270        280        290        300
         |          |          |          |          |          |
GAIIGTLLAL ALIGLIIFCC RKKRREEKYE KEVHHDIRED VPPPKSRTST ARSYIGSNHS

       310        320        330        340        350        360
         |          |          |          |          |          |
SLGSMSPSNM EGYSKTQYNQ VPSEDFERTP QSPTLPPAKV AAPNLSRMGA IPVMIPAQSK
```

DGSIV

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ScanProsite, MotifScan

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The Korean ExPASy site, **kr.expasy.org**, is temporarily not available.